## 

	A=SEQ ID NO: 1 B=SEQ ID NO: 3 D=SEQ ID NO: 2 C= SEQ ID NO: 4	
1533	TGITTGCCTTTTGTTTTCATTGCACGTGAAAAAAGAGGCTGTGTGAATTTTAGAAACTACAAATATAGAATTTTGATTCAACA	.: .: D::
1440	CAAAATAAACGTGTATTTATTACATTCCTCCTTTGTTGAGGTGCAAGGAGTGTAAATGTATTTTTAAAGAATGTTAGAAAAGAAACCATTTCCTTTCATAGGCATGGCAATTC	4 B
1320	TOSTACTOTCCCAAGTGCCGGGGGAGAACGAGAAGACCATGGACAAAAGCCCTGGAGAAATCCAAAAAAGAGAGGCTTACAAGG <u>TAG</u> TTTGTGGACAGGGCCTGGTGGAGGA	.: ä
•	ACCTACTCTCTCTCCAACCAACCAACATCATCGGCACAACGACGACGACGAGTCCCCATCGAGTGCTTCCTCGTCGGGGGCTCCAATCATAAACCCAAGGGGCAAG	A: B/C: D:
1080	GGGGGCTCGGGGACAAGGAGAAGACCTCCAAGAAGAAGACCTCCCAAGGCTCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGAAGCCCAAGGAAGCC	\ B,C; D;
960	GCGGACAGGCCCAAAGGCGAGCCGAGCTGACAACCCCAACAGCGTCACGGCGCAAACGAGAAAACGTGAGAAACGTGAGAACCAACAACCAAC	A: B/C: D:
840	ATCGTGAGCCAGATGGTGGTGGTGGAGAACCGCCAGCACGAGATGGACAGGTGGAGCTGTTCGAGGCGCAGCTGGGCGACACAGCGGGCAACAGCCTGGC	A: B/C: D:
<b>)</b> .	CTAGACGAGTGCTACGAGGCGCGCGCGCGCGCGCGCGCGC	ääöä
9009	CACCTGSTGAACTATGTGGAGGACTACCTGGAGTCCATCGAGCTGCCTTTCGACTTGCAGAAATGTCTGGCTGATGCGGGAGATCGAAGAGGAGATCCTGAAGGAG CCTGAAGGTGTCCCCTCCGCGACCCTCTGGAAAAAGTGACAGGCCAAGGCCACCCCCCCC	ά ä ΰ ä
480	TGCNITITGCAGTGCTATTITTGAGGGGGGGGGGGGGGGGGGGG	<b>ដ</b> ី គី ប៉ូ ជ៉ូ
120 240 360	GOTITICCACGITIGACAAGITGCGCCCCGGGGGGGGGGCGCCCCTTCCCCCTCCCCT	# # # O

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ING2:	\ AAAGCGTTCTCGGCGGCAGCGAACAACTAGAACCGTGAGAACGCGTCCAGCAACCGCGACCCACGACGACGTCA	75
ING1 (D):	C\\GA	
ING2:	CCTCGGGCACGCCCAAGGAGAAGAAGCCCAGACCTCTAAGAAGAAGCAGGGCTCCATGGCCAAGGCGTAGCGGC	150
ING1 (D):	A	
ING2:	AGGCGTCCCCGCAGACCTCCCCATCGACCCCAGCGAGCCCTCCTACTGG	201
ING1 (D):	\TCAAGTCTGTGCAACCAGGTCTCCTATGGG.	
ING2:	AGATGATCCGCTGCGACAACGAATGCCCCATCGAGTGGTTCCGCTTCTCGTGTGTGAGTCTCAACCATAAAC	273
ING1 (D):	G	
ING2:	CAAAGCGCAAGTGGTACTGTTCCAGATGCCGGGGAAAGAACGATGGGCAAAGCCCTTGAGAAGTCCA	340
ING1 (D):	.CGCA.GGGGAAGACCAA	
ING2:	GAAAAAAACAGGGCTTATAACAGGTAGTTTGGGGACATGCGTCTAATAGTGAGGAGAACAAAATAAGCCAGTGT	415
ING1 (D):	G.G\	
ING2:	GTTGATTACATTGCCACCTTTGCTGAGGTGCAGGAAGTGTAAAATGTATATTTTTAAAGAATGTTGTTAGAGGCC	490
ING1 (D):	A.TAGA.AAA	
ING2:	GGGCGCGGTGGCTCACGQCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGTCGGATCACGAGGTCAGGAGATCG	565
ING1 (D):	CCATT.CT.TCA.AGG.A.G.GGGATT.TGCCTTTTGTTTT.AT.G.TT.TAACAAGA.AGT	
ING2:	agaccatcctggctaacacggtgáaaccccgtctctactaaaaattcaaaaaattagctgggcgtggtggc	640
ING1 (D):	G.T.TG.GGATCAGC.TTTTATA.AAA.AGGTTTGC.CTTG.CTCAGACTGA.TTCTTG	
ING2:	GGGCGCCTGTAGTCCCAGCTATTCGGGAGGCTGAGGCAGGAGAATGGCNTGAACCTGGGAGGTGGAGCTTGCANT	715
ING1 (D):	CGAGGAGGG.GA.T.AACTCA.CCT.ACACATTAA.TGT.G.AAAAAT.TTTCATTA.CTTTTT.ATTTTA	
ING2:	GAGCCAAGGTCGCGCCACTGCACTCQAGCCTGGGCGACAGAGCGAGACTCCATCTTA	772
ING1 (D):	$\mathtt{ATA} ext{-}\dots\mathtt{TAATATTACTTTATG}agantleda$ . $\mathtt{AATTTTTTTA}$ . $\mathtt{TT}$ . $\mathtt{GCCA}$ . $\mathtt{GTCG}$ . $\mathtt{CA}$ .	

ING 2 = SEQ 10 NO: 8 ING 1(D) = SEQ 10 NO: 2 (part)

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SEB ID NO. 15

 $\texttt{CTCGTGCCGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGA} \underline{\textbf{ATG}} \texttt{AAAGTTTCTATTCCAACTAAAGCC}$ TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAGCCTGC ATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAGAGTCTC TGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCCAAGGCTACACATCAAAAAGAAATAGATAAAAT AAAT GAAAATTAGAAGAGTCTCCTGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTT  $\mathtt{CTATT} \dot{\boldsymbol{\chi}} \mathtt{CAACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCA}$ TCTGCC\TCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGA ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAGAAGGTTGAAGAAAATTCTT AAAGAAATĠĢATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTATCAAAAATCTTGGATACAGT TCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAAC AAATGAAAAAQAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTA GAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGA GAAGAGAAGAAATGCCGATATATTAAAT AAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGC ATAGGAAAGAGTTÀGAACAACAACAACAACAACACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG AGTGTAGAAAGTAA TTGAATCAGGTT TCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAA TTGCATGTTGAAAAA GAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGG AAAAGGAAAATAAATA&TTTGAGGACATTAAAGATTTTAAAAGAAAGAATGCTGAACTTCAGATGACC CTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTTAAAGTTCTGAT TTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAA AGTCAAGAACCTGCTTTCCACATTGCAGSAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAG TAGTACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGC  ${\tt CTAAAAATTAATCTCAATTATG} {\tt CAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC}$ AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGAT NATGTGAACAACACTGANCAGCAGGAGTCTCTAGATCAGAATTATTTCAACTACAAAGCAAAAA  $\mathtt{TATGTGGCTTCAACAGCAATTAGTT}_{\mathsf{C}}\mathtt{ATGCACATAANGAAAGCTGACAACAAAAGCAAGATAACAATT}$ GATNTTCATTNTCTTGAGAGGAAAA TGCNCATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNAT 

MKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLRADEILPSESKQKDYE ESSWDSESLCETVSQKDVCLPKATHQKEIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQT FKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLRADQMFPSESKQKKVEENSWDSESLRETVSQKD VCVPKATHQKEMDKISGKLEDSTSLSKILDTVHSCERARELQKDHCEQRTGKMEQMKKKFCVLKKKLS EAKEIKSQLENQKVKWEQELCSVRLTLNQEEEKRRNADILNEKIREELGRIEEQHRKELEVKQQLEQA LRIQDIELKSVESNLNQVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKEKQDKEILEAEIESHHPRLASAVQD HDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTD.

## SEQ ID NO. 2

,GAGTAACCCGATAA1\ATGCCGTTGTGCACGGCGACGAGAATTCCCAGATATAGCAGTAGCAGTGATCCCGGGCCT GTGGCTCGGGGCCGGGCTGCAGTTCGGACCGCCTCCCGCGACCCGCGGGGCCGGCTCGGAGACAGTTTCAGGCC GCATCTTTGCTGACCC&AGGGTGGGGCCGCGTGGCCGTGGAAACAGATCCTGAAGGAGCTAGACGAGTGCTAC agccaggagctgggcgachagaagatccagatcgtgagccagatggtggagctggtggagaaccgcacgcggcag GTGGACAGCCACGTGGAGGTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGC GCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGCCCAACAGCAAGCGCTCACGGCGGCAGCGCAAC AACGAGAACCGTGAGAACGACCACGACCACGACCACGCGCGCCTCGGGCACACCCAAGGAGAAGAAG GACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCGGCTGCGACAACGACGAG TGCCCCATCGAGTGGTTCCACTTCTCGTGCGTGGGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAG TGCCGGGGGGAGAACGAGAAGACCAAAAGCCQTGGAGAAATCCAAAAAAGAGAGGGCTTACAACAGGTAG TTTGTGGACAGGCGCCTGGTGTGAGGACAAAAT AAACCGTGTATTTATTACATTGCTGCCTTTGTTGAGGTG CAAGGAGTGTAAAATGTATATTTTAAAAGAATGTTAGAAAAGGAACCATTCCTTTCATAGGGATGGCAGTGATTC TGTTTGCCTTTTGTTTTCATTGGTA\(\alpha\)ACGTGTAAC\(\alpha\)AGAAAGTGGTCTGTGGATCAGCATTTTAGAAACTACAAA  $\verb|TTAAATGTGGAAGGAAAATATTTCATI\| A GCTTTTT | | A TTTTAATACAAGTAATATTATTACTTTATGAACAATTT$ TTTTTAATTGGCCATGTCGCCAAAAATACAGCCTAAAGTAAATGTGTTTCTTGCTGCCATGATGTATATCCATAT AACAATTCAGTAACAAAGGTTTAAAGTT¶GAAGATT¶TTTTTTAAAAAGGTTAAAGGTTAAATTTTACATGACAG ATATTTTATCTATTGGCCTGTTCCCCAAATGGCCATTTTAAAATGCTTG&GTACACTTCTCTTAAGTGGTCTAGT CAAGGAACCTCAAGTCATGCTTTTGCTAT¢ACCAATCATAGTGTACCCATCTTTAATTTATATCAGGTGTATAAA TGTACATTTCCAAATGAACTTGCACTGTAATATTATAATTGGAAGTGCAGTCAGCAGTAGCTGTCGGAGCTAATG auCACAATTATGTGCAAAGGTGTGCTTCCTGdTGTATGTGAGCTGTAAAAATGTTACGTGAAGAAATAAATGAAAC TTGGCCAGTTTGTTCCTCTAGTAGTATTTTAATTTTGACATAAGTAACTTTTAAAATTTGTCTTAAAAATTTAT  $\mathtt{ACACCAGCAATTTAGACAAAGCCTTAAGCAAA}$ TTTTGTATTATTGTTCTCACTTATTATTAATAATGAAGTAGAA GTTACTTAATTGCCAGCAAATAAATACGTGTCAAAAAAGAATCTGTATTCAGACCCCTGGGGTCAGGAAATTACT GTTTCAGCGGCACCCCAAAAAAAAAAAAAAAAAAAAA

gi|2183221|gb|AAB60879.1| p33ING1 (\$\mathcal{GO} ID NO:|\mathcal{Z}\)
MPLCTATRIPRYSSSSDPGPVARGRGCSSDRLPRPAGPARRQFQAASLLTRGWGRAWPWKQILKELDECY
ERFSRETDGAQKRRMLHCVQRALIRSQELGDEKIQIVSOMVELVENRTRQVDSHVELFEAQQELGDTVGN
SGKVGADRPNGDAVAQSDKPNSKRSRRQRNNENRENASSNHDHDDGASGTPKEKKAKTSKKKKRSKAKAE
REASPADLPIDPNEPTYCLCNQVSYGEMIGCDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKTMD
KALEKSKKERAYNR

D:	MPLCTATRIPRYSSS	15
A:	MLSPANGEQLHLVNY\EDYLDSIESLPFDLQRNVSLMREIDAKYQEILKELDECYERFSRETDGAQKRRMLHCVQ	75
B:	MLHCVO	6
C:	MEILKELDECYERFSRETDGAOKRRMLHCVO	31
D:	SDPGPVARGRGCSSDRLARPAGPARRQFQAASLLTRGWGRAWPWKQILKELDECYERFSRETDGAQKRRMLHCVQ	90
A:	RALIRSQELGDEKIQIVSQMVELVENRTRQVDSHVELF <b>E</b> AQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	150
B:	RALIRSQELGDEKIQIVSQMVELVENRTRQVDSHVELFEAQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	156
C:	RALIRSQELGDEKIQIVSQM\ELVENRTRQVDSHVE\fEAQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	106
D:	RALIRSQELGDEKIQIVSQMV\LVENRTRQVDSHV\LFEAQQELGDTVGNSGKVGADRPNGDAVAQSDKPNSKRS	165
A:	RRQRNNENRENASSNHDHDDGA\$GTPKEKKAKTSKKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	225
B:	RRQRNNENRENASSNHDHDDGASGTPKEKKAKTSKKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	231
C:	RRORNNENRENASSNHOHDDGASGTPKEKKAKTSKKKKRSKAKAEREASPADLPIDPNEPTYCLCNOVSYGEMIG	161
D:	RRQRNNENRENASSNHDHDDGASG\TPKEKKAKT\\$KKKKRSKAKAEREASPADLPIDPNEPTYCLCNQVSYGEMIG	240
A:	CDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKTMDKALEKSKKERAYNR.	279
B:	CDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGEN <del>SKIMDKAŁEK</del> SKKERAYNR.	210
C:	CDNDECPIEWFHFSCVGLNHKPKGKWXCPKCRGENEKTMDKALEKSKKERAYNR.	235
D:	CDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGENEKTMDKALEKSKKERAYNR.	294
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A = 5EQ ID NO. 5 B = SEQ ID NO. 6 C = SEQ ID NO. 7 D = SEQ ID NO. 17